AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings of claims in the application.

Listing of claims

1. (Currently amended) A method for identifying a human ~~an individual~~ who has an altered risk for developing coronary stenosis, comprising detecting a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 19350 in a nucleic acid sample from said human, wherein the presence of G at position 101 of SEQ ID NO: 19350 indicates said human is at an increased risk of developing coronary stenosis, and the presence of A at position 101 of SEQ ID NO: 19350 indicates said human is at a decreased risk of developing coronary stenosis ~~in any one of the nucleotide sequences of SEQ ID NOS:1-697 and 1395-67,771 in said individual's nucleic acids, wherein the presence of the SNP is correlated with an altered risk for stenosis in said individual~~.

2. – 5. (Canceled)

6. (Original) The method of claim 1 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

7. – 20. (Canceled)

21. (Currently amended) A method of detecting a single nucleotide polymorphism (SNP) in a nucleic acid molecule, comprising contacting a test sample with a reagent which specifically hybridizes to a SNP as represented by position 101 of SEQ ID NO: 19350 ~~in any one of the nucleotide sequences of SEQ ID NOS:1-697 and 1395-67,771~~ under stringent hybridization conditions, and detecting the formation of a hybridized duplex.

22. (Original) The method of claim 21 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

23. – 24. (Canceled)

25. (New) The method of claim 1, wherein the SNP to be detected is located at position 79090 of SEQ ID NO: 12227.

26. (New) The method of claim 1, wherein the SNP to be detected is located in the LPA gene.

27. (New) The method of claim 1, wherein the detection is carried out by using a set of detection reagents comprising the oligonucleotide sequences of SEQ ID NO: 68222, SEQ ID NO: 68223, and SEQ ID NO: 68224.

28. (New) A method for identifying a human who has an increased risk for developing coronary stenosis, comprising detecting a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 19350 in a nucleic acid sample from said human, wherein the presence of G at position 101 of SEQ ID NO: 19350 indicates said human is at an increased risk of developing coronary stenosis.

29. (New) The method of claim 28 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

30. (New) The method of claim 28, wherein the SNP to be detected is located at position 79090 of SEQ ID NO: 12227.

31. (New) The method of claim 28, wherein the SNP to be detected is located in the LPA gene.

32. (New) The method of claim 28, wherein the detection is carried out by using a set of detection reagents comprising the oligonucleotide sequences of SEQ ID NO: 68222, SEQ ID NO: 68223, and SEQ ID NO: 68224.

33. (New) A method for identifying a human who has a decreased risk for developing coronary stenosis, comprising detecting a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 19350 in a nucleic acid sample from said human, wherein the presence of A at position 101 of SEQ ID NO: 19350 indicates said human is at a decreased risk of developing coronary stenosis.

34. (New) The method of claim 33 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

35. (New) The method of claim 33, wherein the SNP to be detected is located at position 79090 of SEQ ID NO: 12227.

36. (New) The method of claim 33, wherein the SNP to be detected is located in the LPA gene.

37. (New) The method of claim 33, wherein the detection is carried out by using a set of detection reagents comprising the oligonucleotide sequences of SEQ ID NO: 68222, SEQ ID NO: 68223, and SEQ ID NO: 68224.